

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:04 ; Search time 29.37 Seconds

(without alignments)
24.190 Million cell updates/sec

Title: US-09-331-631A-39

Perfect score: 54
Sequence: 1 CXXXXXXXXXXXXXXXXCXXC 22

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	40	1 MT1_DROME	P04357 drosophila
2	54	100.0	40	1 MT1_DROSI	P22354 drosophila
3	54	100.0	43	1 MT2_DROME	P11956 drosophila
4	54	100.0	47	1 AGRP_LUCFY	P56568 lufcia cylin
5	54	100.0	55	1 M84C_DROME	O01644 drosophila
6	54	100.0	57	1 MT2_SCYSE	P02806 scylla serr
7	54	100.0	58	1 MT1_HOMAN	P29499 homarus ame
8	54	100.0	58	1 MT1_SCYSE	P02805 scylla serr
9	54	100.0	58	1 MT2_CALSI	P55950 callinectes
10	54	100.0	58	1 MT_ASTFL	P55951 astacus flu
11	54	100.0	58	1 MT_CARMA	P55948 carcinus ma
12	54	100.0	58	1 MT_POTPO	P55952 potamon pot
13	54	100.0	59	1 MT1_CALSI	P55949 callinectes
14	54	100.0	61	1 MT1B_HUMAN	P07438 homo sapien
15	54	100.0	63	1 M84A_DROME	O01642 drosophila
16	54	100.0	64	1 MTA_STRPU	P04734 strongyloce
17	54	100.0	64	1 MTCU_HELPO	P55947 helix pomat
18	54	100.0	64	1 MT_STENE	P55953 stercorinus
19	54	100.0	65	1 MT_PARLI	P80367 paracentrot
20	54	100.0	66	1 MTCO_HELPO	P33187 helix pomat
21	54	100.0	66	1 MTA_ARIR	P55946 arlanta arb
22	54	100.0	67	1 MTA_SPHGR	O26497 sphaerechin
23	54	100.0	67	1 MTA_SPHGR	O26496 sphaerechin
24	54	100.0	68	1 M84D_DROME	O01645 drosophila
25	54	100.0	71	1 MT21_MYTED	P80251 mytilus edu
26	54	100.0	71	1 MT22_MYTED	P80252 mytilus edu
27	54	100.0	71	1 MT23_MYTED	P80253 mytilus edu
28	54	100.0	74	1 M84B_DROME	O01643 drosophila
29	54	100.0	74	1 MT_CRAVI	P23038 crassostrea
30	54	100.0	74	1 MDNM_MOUSE	O62477 mus musculu
31	54	100.0	74	1 MDNM_RAT	P14730 ratius norv
32	54	100.0	95	1 EP4_RABIT	O28631 oryctolagus
33	54	100.0	95	1 YWS6_CAEEL	O10942 caenorhabdi

34	54	100.0	96	1 RS11_LYCES	P47926 lycopersico
35	54	100.0	98	1 GAS1_ARATH	P46689 arabidopsis
36	54	100.0	99	1 GAS2_ARATH	P46688 arabidopsis
37	54	100.0	99	1 GAS3_ARATH	P46687 arabidopsis
38	54	100.0	105	1 INB4_CAEEL	O23430 caenorhabdi
39	54	100.0	106	1 GAS4_ARATH	P46680 arabidopsis
40	54	100.0	106	1 INB1_CAEEL	O09626 caenorhabdi
41	54	100.0	110	1 IBP_CARCR	P00993 caretta car
42	54	100.0	112	1 GST1_LYCES	P27057 lycopersico
43	54	100.0	124	1 INB5_CAEEL	P56174 caenorhabdi
44	54	100.0	124	1 CHH2_BOMMO	P05687 bombyx mori
45	54	100.0	124	1 EP4_CANFA	O28894 canis famli

ALIGNMENTS

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RESULT 1
ID MT1_DROME STANDARD; PRT; 40 AA.
AC P04357; Q9VH67;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE METALLOTHIONEIN 1 (MT-1).
GN MTNA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6165787; PubMed=3007277;
RA Maroni G., Otto E., Lastowski-Perry D.;
RT "Molecular and cytogenetic characterization of a metallothionein gene
of Drosophila."
RL Genetics 112:493-504(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=65105016; PubMed=2578462;
RA Lastowski-Perry D., Otto E., Maroni G.;
RT "Nucleotide sequence and expression of a Drosophila metallothionein."
RL J. Biol. Chem. 260:1527-1530(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=66219988; PubMed=3086075;
RA Maroni G., Lastowski-Perry D., Otto E., Watson D.;
RT "Effects of heavy metals on Drosophila larvae and a metallothionein
cDNA."
RL Environ. Health Perspect. 65:107-116(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=68029907; PubMed=2822463;
RA Maroni G., Otto E., Lastowski-Perry D., Price D.H.;
RT "The metallothionein gene of Drosophila."
RL Experientia Suppl. 52:385-392(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92201681; PubMed=1802803;
RA Theodore L., Ho A.-S., Maroni G.;
RT "Recent evolutionary history of the metallothionein gene Mtn in
Drosophila."
RL Genet. Res. 58:203-210(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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RA Abiril J.F., Agbavanyi A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L.U., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhanderi D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck H., Butler J., Brooksstein P., Brottler P.,
RA Burtils K.C., Busam D.A., Butler H., Cadieu E., Centler A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dopp L.E., Downes M., Dugan-Hochs S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibsenwang C.,
RA Jalali M., Kaluston F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McInneson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J.J., Mosheriff A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Neilson D.R., Nelson K.A., Nixon K., Nusserken D.R., Pacible J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Sliden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtka S., Teclor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [17]
RN
RP REGULATION AND EXPRESSION.
RX MEDLINE=91012582; PubMed=1976815;
RA Silar P., Theodorou L., Mokdad R., Errais N.-E., Cadic A., Wegnez M.,
RT "Metallothionein Mto gene of Drosophila melanogaster: structure and
RT regulation." ;
RL J. Mol. Biol. 215:217-224(1990).
CC -I- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
CC ELEMENTS. IT IS THOUGHT TO BE INVOLVED IN DETOXIFICATION
CC PROCESSES.
CC -I- DEVELOPMENTAL STAGE: LATE EMBRYONESIS, LARVA AND ADULT.
CC -I- INDUCTION: STRONGLY INDUCED BY CADMIUM, COPPER AND MERCURY.
CC -I- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.
CC THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
CC METALLOTHIONEINS.
CC -I- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE
CC ONLY 26% SIMILAR.
CC -I- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.
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CC -----
DR EMBL; X03758; CAZ27391.1; -;
DR EMBL; K02314; AAA28681.1; -;
DR EMBL; M27708; AAA28684.1; -;
DR EMBL; M69015; ABA41334.1; -;
DR EMBL; AE003684; AAP54452.1; -;
DR PIR; A03285; SMEF.
DR PIR; A25294; A25294.
DR HSSP; P04355; 4MT2.
DR FLYBASE; FBGN0002868; MTNA.
DR INTERPRO; IPRO009066; -;
DR PRAM; PF02067; Metallothio_5; 1.
DR PRINTS; PR00872; MTDIPTERA.
KW Metal-binding; Chelation; Copper; Cadmium; Zinc; Mercury;
KW Polymorphism.

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FT          VARIANT      40      40      E -> K (IN MTN-33)
SQ          SEQUENCE    40 AA: 3853 MW: 99A2A53CCCAE634A CRC64:
                                Query Match      100.0%; Score 54; DB 1; Length 40;
                                Best Local Similarity 18.2%; Pred. NO. 38;
                                Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
Oy          1 CAXXCXXXXXXXXXXXXC 22
Db          5 CGSGCKCASQATKSGCNCGSDC 26

RESULT      2
MT1_DROSI   STANDARD:      PRT:      40 AA.
AC          P2254;
DT          01-AUG-1991 (Rel. 19, Created)
DT          01-AUG-1991 (Rel. 19, Last sequence update)
DE          01-OCT-2000 (Rel. 40, Last annotation update)
DE          METALLOTHIONEIN 1 (MT-1).
GN          MTN.
OS          Drosophila simulans (Fruit fly), and Drosophila ananassae (Fruit fly).
OC          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC          Ephydroidea; Drosophilidae; Drosophila.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          SPECIES=D.SIMULANS;
RC          MEDLINE=91169270; PubMed=1981765;
RA          Lange B.W., Langley C.H., Stephan W.H.;
RL          "Molecular evolution of Drosophila metallothionein genes.";
RL          Genetics 126:921-932(1990).
RN          [2]
RP          SEQUENCE FROM N.A.
RC          SPECIES=D.SIMULANS;
RC          MEDLINE=92201681; PubMed=1802803;
RA          Theodore L., Ho A.-S., Maroni G.;
RT          "Recent evolutionary history of the metallothionein gene Mtn in
RT          Drosophila.";
RL          Genet. Res. 58:203-210(1991).
RN          [3]
RP          SEQUENCE FROM N.A.
RC          SPECIES=D.ANANASSAE;
RC          MEDLINE=95095041; PubMed=8001781;
RA          Stephan W., Rodriguez V.S., Zhou B., Parsch J.;
RT          "Molecular evolution of the metallothionein gene Mtn in the
RT          melanogaster species group: results from Drosophila ananassae.";
RL          Genetics 138:135-143(1994).
CC          -I- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
CC          ELEMENTS. IT IS THOUGHT TO BE INVOLVED IN DETOXIFICATION
CC          PROCESSES.
CC          -I- DEVELOPMENTAL STAGE: LATE EMBRYOGENESIS, LARVA AND ADULT.
CC          -I- INDUCTION: STRONGLY INDUCED BY CADMIUM, COPPER AND MERCURY.
CC          -I- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.
CC          THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
CC          METALLOTHIONEINS.
CC          -I- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE
CC          ONLY 26% SIMILAR.
CC          -I- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.
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CC          or send an email to license@isb-sib.ch).
CC          -----
DR          EMBL, M55407; AAA03345.1; -
DR          EMBL, M69016; AAI1987.1; -
DR          EMBL, S75822; AAB32801.1; -
DR          PIR: A45892; A45892.

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DR HSSP: P04355; 4MT2.
 DR FLYBASE: FBgn0012845; Dsim\MtnA.
 DR FLYBASE: FBgn0013782; Dana\MtnA.
 DR INTERPRO: IPR000966; -.
 DR PFAM: PF02067; Metallothio_5; 1.
 DR PRINTS: PR00872; MTDIPTERA.
 DR Metal-binding; Chelation; Copper; Cadmium; Zinc.
 KW Metal-binding; Chelation; Copper; Cadmium; Zinc.
 SQ SEQUENCE 40 AA; 3852 MW; 9182A53CCCAE634A CRC64;

Query Match 100.0%; Score 54; DB 1; Length 40;
 Best Local Similarity 18.2%; Pred. No. 38;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXCXXXXXXXXXXCXXC 22
 Db 5 CGSCKRCASQATKGCNCSCSDC 26

RESULT 3
 MT2_DROME STANDARD; PRT; 43 AA.
 AC P11956; O9VDM2;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE METALLOTHIONEIN 2 (MT-2).
 GN MTNB OR MTO.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=87204190; PubMed=3106973;
 RA Moked R., Debec A., Wegnez M.;
 RT "Metallothionein genes in Drosophila melanogaster constitute a dual
 system";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2658-2662(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 3-27.
 RC STRAIN=OREGON-R;
 RX MEDLINE=91012582; PubMed=1976815;
 RA Sillar P., Theodore L., Moked R., Errais N.-E., Cadic A., Wegnez M.;
 RT "Metallothionein Mto gene of Drosophila melanogaster: structure and
 regulation";
 RL J. Mol. Biol. 215:217-224(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amannites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang X., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 Burdits K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glisick A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison K.J., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., Meled M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosureil A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
 CC ELEMENTS. THOUGHT TO BE INVOLVED IN METAL ION HOMEOSTASIS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY IN EMBRYONIC AND
 CC LARVAL STAGES.
 CC -1- INDUCTION: STRONGLY INDUCED BY CADMIUM, COPPER AND MERCURY.
 CC -1- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.
 CC THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
 CC METALLOTHIONEINS.
 CC -1- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE
 CC ONLY 26% SIMILAR.
 CC -1- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.
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 CC -----
 CC DR EMBL: M16250; AAA28683.1; -
 CC DR EMBL: X52098; CAA36318.1; -
 CC DR EMBL: AE003730; AAP55768.1; -
 CC DR PIR: S14706; SMPF2.
 CC DR FLYBASE: FBgn0002869; MtnB.
 CC DR INTERPRO: IPR000966; -
 CC DR PFAM: PF02067; Metallothio_5; 1.
 CC DR PRINTS: PR00872; MTDIPTERA.
 CC KW Metal-binding; Chelation; Copper; Cadmium; Zinc.
 CC SEQUENCE 43 AA; 4525 MW; 5EE0CF9171BD9A97 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 43;
 Best Local Similarity 18.2%; Pred. No. 40;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXCXXXXXXXXXXCXXC 22
 Db 6 CGTNCOCASQKCDNCAKNKDC 27

RESULT 4
 AGRP_LUFCY STANDARD; PRT; 47 AA.
 ID AGRP_LUFCY
 AC P56568;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 6.5 KDA ARGININE/GUTAMATE-RICH POLYPEPTIDE (6.5K-AGRP).
 OC Lufka cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Cucurbitales; Cucurbitaceae; Lufka.
 RN [1]
 RP SEQUENCE.
 RC TTSUE=SEED;

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RA MEDLINE=97357433; PubMed=9214759;
RA Kimura M., Park S.-S., Sakai R., Yamasaki N., Funatsu G.;
RT "Primary structure of 6,5k-arginine/glutamate-rich polypeptide from
RT the seeds of sponge gourd (Luffa cylindrica).";
RA Biosci. Biotechnol. Biochem. 61:984-988(1997).
CC
CC -1- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON
CC RESERVES DURING GERMINATION AND SEEDLING GROWTH.
CC -1- MASS SPECTROMETRY: MW=5693.39; METHOD=MALDI.
CC -1- SIMILARITY: SOME, TO 7S SEED STORAGE PROTEINS.
CC Seed storage protein.
KW DISULFID 12 33
FT DISULFID 16 29
SQ SEQUENCE 47 AA; 5698 MW; 588B0BC82273AC05 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 47;
Best Local Similarity 18.2%; Pred. No. 43;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
DB 12 CRYRCQVAEHGVERORRCQVC 33

RESULT 5
M84C_DROME STANDARD; PRT: 55 AA.
AC 001644; 09VIA0;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN M84C.
GN M84C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydrotidae; Drosophilidae; Drosophila.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92102953; PubMed=1684716;
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abtill J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bernan B.P., Bhanderi D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Buttis K.C., Busan D.A., Butler H., Cadieu E., Genter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman J.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwan C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sienkiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X67703; CAA47939.1; -
DR EMBL; AE003672; AAF54025.1; -.
DR HSSP; P01180; INPO.
DR FLYBASE; FBgn004174; M84C.
KW Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 55 AA; 5225 MW; 95A12F3AEC88B0DC CRC64;

Query Match 100.0%; Score 54; DB 1; Length 55;
Best Local Similarity 18.2%; Pred. No. 47;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
DB 15 CGPCCGPGCGPCGSCGCGC 36

RESULT 6
M84C_DROME STANDARD; PRT: 57 AA.
AC P02806;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II).
OS Scylla serrata (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Scylla.
RN (1)
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lerch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins I and
RT 2."
RA J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR; A03284; SMK25.
CC HSSP; P55949; 10MF.
DR INTERPRO; IPR002045; -

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DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28
FT METAL 29 57 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BAA3611 CRC64;
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Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 18.2%; Pred. No. 48;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CXXXXXXXXXXXXXXXXX 22
Db 16 CKTGCKTSCRCPCPCGCCSGC 37
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RESULT 7
MT1_HOMAM STANDARD; PRT; 58 AA.
ID MT1_HOMAM
AC P29499;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (CUMT-1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
RN (1)
RP SEQUENCE.
RC TISSUE=HEPATOPANCREAS;
RX MEDLINE=89215793; PubMed=2709004;
RA Brouwer M., Winge D.R., Gray W.R.;
RT Structural and functional diversity of copper-metalllothioneins from
RL the American lobster Homarus americanus. J. Inorg. Biochem. 35:289-303(1989).
RN (2)
RP STRUCTURE BY NMR.
RX MEDLINE=94318629; PubMed=8043573;
RA Zhu Z., DeRose E.F., Mullen G.P., Petering D.H., Shaw C.F. III;
RT Sequential proton resonance assignments and metal cluster topology
RL of lobster metalllothionein-1. J. Biochemistry 33:8858-8865(1994).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF
LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.
CC CLASS 1 MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION
OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN
CC TO BIND CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR; A37039; A37039.
DR HSSP; P55949; IDMF.
DR INTERPRO; IPR002045; -.
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DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 28
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 5975 MW; 176ABAA60A32F96 CRC64;
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Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 18.2%; Pred. No. 49;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CXXXXXXXXXXXXXXXXX 22
Db 16 CKTGCKTSCRCAPCEKCTSGC 37
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RESULT 8
MT1_SCYSE STANDARD; PRT; 58 AA.
ID MT1_SCYSE
AC P02805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (MT-I).
OS Scyllia serrata (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Scylla.
RN (1)
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lerch K., Ammer D., Olafson R.W.;
RT "Crab metalllothionein. Primary structures of metalllothioneins 1 and
RT 2."
RL J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS 1 MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR; A03283; SKKDIS.
DR HSSP; P55949; IDMF.
DR INTERPRO; IPR002045; -.
DR INTERPRO; IPR003019; -.
DR PFAM; PF00131; metalchio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
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FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 6001 MW; CE8A24C590B027B8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 58;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXXXCXXC 22
16 CKEGCCTCSCRCSPCKCSCGC 37

RESULT 9
MT2_CALSI STANDARD; PRT; 58 AA.
AC P55950;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
RN [1]
RP MEDLINE=96033062; PubMed=7487904;
RA Browner M., Engthild J., Hoexum-Brouwer T., Thogersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
(Callinectes sapidus) metallothionein isoforms."
RL Biochem. J. 311:617-622(1995).
CC -1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CC CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; 1DMD.
DR INTERPRO: IPR002045; -
DR INTERPRO: IPR003019; -
DR PFAM: PF00131; metalthio: 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 5911 MW; 576365B3BE5C7122 CRC64;

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FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN MT-IIA).
SQ SEQUENCE 58 AA; 6287 MW; EF679CB94975C5F0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 58;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXXXCXXC 22
17 CKKGCKKRCRCPCDKCSCSEC 38

RESULT 10
MT_ASTFL STANDARD; PRT; 58 AA.
AC P55951;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE METALLOTHIONEIN (MT).
OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Astacidae; Astacus.
RN [1]
RP SEQUENCE.
RC TISSUE=MIDGUT;
RX MEDLINE=97079279; PubMed=8921011;
RA Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
special emphasis on freshwater and semi-terrestrial species."
RL Biochem. J. 319:999-1003(1996).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
CC ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
CC METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MW=5910.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; 1DMD.
DR INTERPRO: IPR002045; -
DR INTERPRO: IPR003019; -
DR PFAM: PF00131; metalthio: 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
FT FT CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 5911 MW; 576365B3BE5C7122 CRC64;

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Query Match

100.0%; Score 54; DB 1; Length 58;

Best Local Similarity 18.2%; Pred. No. 49;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
17 CKTGCVCTSCRCSPCKCTSGC 38

RESULT 11

MT_CARMA
ID MT_CARMA STANDARD; PRT: 58 AA.
AC P55948;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP TISSUE=MIDGUT;
RC MEDLINE=9415337; PubMed=8110201;
RA Pedersen K.L., Pedersen S.N., Hoejrup P., Andersen J.S.,
Roepstorff P., Knudsen J., Depledge M.H.;
RT "Purification and characterization of a cadmium-induced
metallothionein from the shore crab Carcinus maenas (L.).";
RL Biochem. J. 297:609-614(1994).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
OF HEAVY-METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; IDMD.
DR INTERPRO: IPR002045; -;
DR PFM: PF00131; metalchio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KM Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 6133 MW; 0167CDA2B9C9731D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 18.2%; Pred. No. 49;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
17 CKAGCKCTSCRCSPCKCKSSGC 38

RESULT 12

MT_POTPO
ID MT_POTPO STANDARD; PRT: 58 AA.
AC P55952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Potamon potamos.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Geryonidae; Potamon.
RN [1]
RP TISSUE=MIDGUT;
RC MEDLINE=97079279; PubMed=8921011;
RA Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:989-1003(1996).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MW=6156.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; IDMD.
DR INTERPRO: IPR002045; -;
DR PFM: PF00131; metalchio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KM Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29
FT METAL 30 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
SQ SEQUENCE 58 AA; 6157 MW; DCB71P9AB4DF779C CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 18.2%; Pred. No. 49;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
17 CKAGCKCTSCRCSPCKCTSEC 38

RESULT 13

MT1_CALSI
ID MT1_CALSI STANDARD; PRT: 59 AA.
AC P55949;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXX 22
 Db 15 CAGCCKCKCKCTCKCKCCSC 36

RESULT 15
 M84A.DROME STANDARD: PRT; 63 AA.
 AC 001642: 09YIA3:
 DT 01-JUL-1993 (rel. 26, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE MALE SPECIFIC SPERM PROTEIN M8784DA.
 GN M8784DA.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=OREGON-R;
 RX MEDLINE=92102953; PubMed=1684716;
 RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
 RA Schaefer M.;
 RT "A cluster of four genes selectively expressed in the male germ line
 of Drosophila melanogaster";
 RL Mech. Dev. 35:143-151(1991).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R.C., Smith T.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -I- TISSUE SPECIFICITY: TESTIS.
 CC -I- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.

CC -I- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
 CC MOTIFS.
 CC -I- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; X67703; CAA47937.1; -.
 CC DR EMBL; AE003672; AAF54022.1; -.
 CC DR HSSP; P01180; INPO.
 CC DR FLYBASE; FBgn0004172; M8184DA.
 CC Spermatoogenesis; Repeat; Multigene family.
 KW SEQUENCE 63 AA; 5806 MW; BF84CD74CBCEFD3F CRC64;
 SQ

Query Match 100.0%; Score 54; DB 1; Length 63;
 Best Local Similarity 18.2%; Pred. No. 52;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXX 22
 Db 29 CGPCGCGCGPCGCGCGCGPC 50

Search completed: March 1, 2001, 16:26:04
 Job time: 401 sec

